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cgctctagcc cggtgggaag ctttcatcca gaaca atg aat ttc ata aag gac	53
Met Asn Phe Ile Lys Asp 1 5	
aat agc cga gcc ctt att caa aga atg gga atg act gtt ata aag caa	101
Asn Ser Arg Ala Leu Ile Gln Arg Met Gly Met Thr Val Ile Lys Gln 10 15 20	
atc aca gat gac cta ttt gta tgg aat gtt ctg aat cgc gaa gaa gta	149
Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val 25 30 35	
aac atc att tgc tgc gag aag gtg gag cag gat gct gct aga ggg atc	197
Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile 40 45 50	
att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt	245
Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu 55 60 65 70	
aaa tcc ctt aag gag tgg aac tat cct cta ttt cag gac ttg aat gga	293
Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu Phe Gln Asp Leu Asn Gly 75 80 85	
caa agt ctt ttt cat cag aca tca gaa gga gac ttg gac gat ttg gct	341
Gln Ser Leu Phe His Gln Thr Ser Glu Gly Asp Leu Asp Asp Leu Ala 90 95 100	
cag gat tta aag gac ttg tac cat acc cca tct ttt ctg aac ttt tat	389
Gln Asp Leu Lys Asp Leu Tyr His Thr Pro Ser Phe Leu Asn Phe Tyr 105 110 115	
ccc ctt ggt gaa gat att gac att att ttt aac ttg aaa agc acc ttc	437
Pro Leu Gly Glu Asp Ile Asp Ile Ile Phe Asn Leu Lys Ser Thr Phe 120 125 130	
aca gaa cct gtc ctg tgg agg aag gac caa cac cat cac cgc gtg gag	485
Thr Glu Pro Val Leu Trp Arg Lys Asp Gln His His His Arg Val Glu 135 140 145 150	
cag ctg acc ctg aat ggc ctc ctg cag gct ctt cag agc ccc tgc atc	533
Gln Leu Thr Leu Asn Gly Leu Leu Gln Ala Leu Gln Ser Pro Cys Ile 155 160 165	
att gaa ggg gaa tct ggc aaa ggc aag tcc act ctg ctg cag cgc att	581
Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser Thr Leu Leu Gln Arg Ile 170 175 180	
gcc atg ctc tgg ggc tcc gga aag tgc aag gct ctg acc aag ttc aaa	629
Ala Met Leu Trp Gly Ser Gly Lys Cys Lys Ala Leu Thr Lys Phe Lys 185 190 195	
ttc gtc ttc ttc ctc cgt ctc agc agg gcc cag ggt gga ctt ttt gaa	677
Phe Val Phe Phe Leu Arg Leu Ser Arg Ala Gln Gly Gly Leu Phe Glu 200 205 210	

FIG. 1A

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acc	ctc	tgt	gat	caa	ctc	ctg	gat	ata	cct	ggc	aca	atc	agg	aag	cag	725
Thr	Leu	Cys	Asp	Gln	Leu	Leu	Asp	Ile	Pro	Gly	Thr	Ile	Arg	Lys	Gln	
215					220					225					230	
aca	ttc	atg	gcc	atg	ctg	ctg	aag	ctg	cgg	cag	agg	gtt	ctt	ttc	ctt	773
Thr	Phe	Met	Ala	Met	Leu	Leu	Lys	Leu	Arg	Gln	Arg	Val	Leu	Phe	Leu	
				235					240					245		
ctt	gat	ggc	tac	aat	gaa	ttc	aag	ccc	cag	aac	tgc	cca	gaa	atc	gaa	821
Leu	Asp	Gly	Tyr	Asn	Glu	Phe	Lys	Pro	Gln	Asn	Cys	Pro	Glu	Ile	Glu	
			250					255					260			
gcc	ctg	ata	aag	gaa	aac	cac	cgc	ttc	aag	aac	atg	gtc	atc	gtc	acc	869
Ala	Leu	Ile	Lys	Glu	Asn	His	Arg	Phe	Lys	Asn	Met	Val	Ile	Val	Thr	
	265						270					275				
act	acc	act	gag	tgc	ctg	agg	cac	ata	cgg	cag	ttt	ggg	gcc	ctg	act	917
Thr	Thr	Thr	Glu	Cys	Leu	Arg	His	Ile	Arg	Gln	Phe	Gly	Ala	Leu	Thr	
	280					285					290					
gct	gag	gtg	ggg	gat	atg	aca	gaa	gac	agc	gcc	cag	gct	ctc	atc	cga	965
Ala	Glu	Val	Gly	Asp	Met	Thr	Glu	Asp	Ser	Ala	Gln	Ala	Leu	Ile	Arg	
295					300					305					310	
gaa	gtg	ctg	atc	aag	gag	ctt	gct	gaa	ggc	ttg	ttg	ctc	caa	att	cag	1013
Glu	Val	Leu	Ile	Lys	Glu	Leu	Ala	Glu	Gly	Leu	Leu	Leu	Gln	Ile	Gln	
				315					320					325		
aaa	tcc	agg	tgc	ttg	agg	aat	ctc	atg	aag	acc	cct	ctc	ttt	gtg	gtc	1061
Lys	Ser	Arg	Cys	Leu	Arg	Asn	Leu	Met	Lys	Thr	Pro	Leu	Phe	Val	Val	
			330					335					340			
atc	act	tgt	gca	atc	cag	atg	ggg	gaa	agt	gag	ttc	cac	tct	cac	aca	1109
Ile	Thr	Cys	Ala	Ile	Gln	Met	Gly	Glu	Ser	Glu	Phe	His	Ser	His	Thr	
		345					350					355				
caa	aca	acg	ctg	ttc	cat	acc	ttc	tat	gat	ctg	ttg	ata	cag	aaa	aac	1157
Gln	Thr	Thr	Leu	Phe	His	Thr	Phe	Tyr	Asp	Leu	Leu	Ile	Gln	Lys	Asn	
	360					365					370					
aaa	cac	aaa	cat	aaa	ggg	gtg	gct	gca	agt	gac	ttc	att	cgg	agc	ctg	1205
Lys	His	Lys	His	Lys	Gly	Val	Ala	Ala	Ser	Asp	Phe	Ile	Arg	Ser	Leu	
375					380					385					390	
gac	cac	tgt	gga	gac	cta	gct	ctg	gag	ggg	gtg	ttc	tcc	cac	aag	ttt	1253
Asp	His	Cys	Gly	Asp	Leu	Ala	Leu	Glu	Gly	Val	Phe	Ser	His	Lys	Phe	
				395				400						405		
gat	ttc	gaa	ctg	cag	gat	gtg	tcc	agc	gtg	aat	gag	gat	gtc	ctg	ctg	1301
Asp	Phe	Glu	Leu	Gln	Asp	Val	Ser	Ser	Val	Asn	Glu	Asp	Val	Leu	Leu	
			410					415					420			
aca	act	ggg	ctc	ctc	tgt	aaa	tat	aca	gct	caa	agg	ttc	aag	cca	aag	1349
Thr	Thr	Gly	Leu	Leu	Cys	Lys	Tyr	Thr	Ala	Gln	Arg	Phe	Lys	Pro	Lys	
		425					430					435				

FIG. 1B

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tat	aaa	ttc	ttt	cac	aag	tca	ttc	cag	gag	tac	aca	gca	gga	cga	aga	1397
Tyr	Lys	Phe	Phe	His	Lys	Ser	Phe	Gln	Glu	Tyr	Thr	Ala	Gly	Arg	Arg	
	440					445					450					
ctc	agc	agt	tta	ttg	acg	tct	cat	gag	cca	gag	gag	gtg	acc	aag	ggg	1445
Leu	Ser	Ser	Leu	Leu	Thr	Ser	His	Glu	Pro	Glu	Glu	Val	Thr	Lys	Gly	
455					460					465					470	
aat	ggt	tac	ttg	cag	aaa	atg	gtt	tcc	att	tcg	gac	att	aca	tcc	act	1493
Asn	Gly	Tyr	Leu	Gln	Lys	Met	Val	Ser	Ile	Ser	Asp	Ile	Thr	Ser	Thr	
				475					480					485		
tat	agc	agc	ctg	ctc	cgg	tac	acc	tgt	ggg	tca	tct	gtg	gaa	gcc	acc	1541
Tyr	Ser	Ser	Leu	Leu	Arg	Tyr	Thr	Cys	Gly	Ser	Ser	Val	Glu	Ala	Thr	
			490					495					500			
agg	gct	gtt	atg	aag	cac	ctc	gca	gca	gtg	tat	caa	cac	ggc	tgc	ctt	1589
Arg	Ala	Val	Met	Lys	His	Leu	Ala	Ala	Val	Tyr	Gln	His	Gly	Cys	Leu	
		505					510					515				
ctc	gga	ctt	tcc	atc	gcc	aag	agg	cct	ctc	tgg	aga	cag	gaa	tct	ttg	1637
Leu	Gly	Leu	Ser	Ile	Ala	Lys	Arg	Pro	Leu	Trp	Arg	Gln	Glu	Ser	Leu	
520						525					530					
caa	agt	gtg	aaa	aac	acc	act	gag	caa	gaa	att	ctg	aaa	gcc	ata	aac	1685
Gln	Ser	Val	Lys	Asn	Thr	Thr	Glu	Gln	Glu	Ile	Leu	Lys	Ala	Ile	Asn	
535					540					545					550	
atc	aat	tcc	ttt	gta	gag	tgt	ggc	atc	cat	tta	tat	caa	gag	agt	aca	1733
Ile	Asn	Ser	Phe	Val	Glu	Cys	Gly	Ile	His	Leu	Tyr	Gln	Glu	Ser	Thr	
				555				560						565		
tcc	aaa	tca	gcc	ctg	agc	caa	gaa	ttt	gaa	gct	ttc	ttt	caa	ggt	aaa	1781
Ser	Lys	Ser	Ala	Leu	Ser	Gln	Glu	Phe	Glu	Ala	Phe	Phe	Gln	Gly	Lys	
			570					575					580			
agc	tta	tat	atc	aac	tca	ggg	aac	atc	ccc	gat	tac	tta	ttt	gac	ttc	1829
Ser	Leu	Tyr	Ile	Asn	Ser	Gly	Asn	Ile	Pro	Asp	Tyr	Leu	Phe	Asp	Phe	
		585					590					595				
ttt	gaa	cat	ttg	ccc	aat	tgt	gca	agt	gct	ctg	gac	ttc	att	aaa	ctg	1877
Phe	Glu	His	Leu	Pro	Asn	Cys	Ala	Ser	Ala	Leu	Asp	Phe	Ile	Lys	Leu	
	600					605					610					
gac	ttt	tat	ggg	gga	gct	atg	gct	tca	tgg	gaa	aag	gct	gca	gaa	gac	1925
Asp	Phe	Tyr	Gly	Gly	Ala	Met	Ala	Ser	Trp	Glu	Lys	Ala	Ala	Glu	Asp	
615					620					625					630	
aca	ggt	gga	atc	cac	atg	gaa	gag	gcc	cca	gaa	acc	tac	att	ccc	agc	1973
Thr	Gly	Gly	Ile	His	Met	Glu	Glu	Ala	Pro	Glu	Thr	Tyr	Ile	Pro	Ser	
				635					640					645		
agg	gct	gta	tct	ttg	ttc	ttc	aac	tgg	aag	cag	gaa	ttc	agg	act	ctg	2021
Arg	Ala	Val	Ser	Leu	Phe	Phe	Asn	Trp	Lys	Gln	Glu	Phe	Arg	Thr	Leu	
			650					655					660			

FIG. 1C

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gag gtc aca ctc cgg gat ttc agc aag ttg aat aag caa gat atc aca	2069
Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn Lys Gln Asp Ile Thr	
665 670 675	
tat ctg ggg aaa ata ttc agc tct gcc aca agc ctc agg ctg caa ata	2117
Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser Leu Arg Leu Gln Ile	
680 685 690	
aag aga tgt gct ggt gtg gct gga agc ctc agt ttg gtc ctc agc acc	2165
Lys Arg Cys Ala Gly Val Ala Gly Ser Leu Ser Leu Val Leu Ser Thr	
695 700 705 710	
tgt aag aac att tat tct ctc atg gtg gaa gcc agt ccc ctc acc ata	2213
Cys Lys Asn Ile Tyr Ser Leu Met Val Glu Ala Ser Pro Leu Thr Ile	
715 720 725	
gaa gat gag agg cac atc aca tct gta aca aac ctg aaa acc ttg agt	2261
Glu Asp Glu Arg His Ile Thr Ser Val Thr Asn Leu Lys Thr Leu Ser	
730 735 740	
att cat gac cta cag aat caa cgg ctg ccg ggt ggt ctg act gac agc	2309
Ile His Asp Leu Gln Asn Gln Arg Leu Pro Gly Gly Leu Thr Asp Ser	
745 750 755	
ttg ggt aac ttg aag aac ctt aca aag ctc ata atg gat aac ata aag	2357
Leu Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys	
760 765 770	
atg aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg	2405
Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu	
775 780 785 790	
aag aag atg tgt tta ttt cat ttg acc cac ttg tct gac att gga gag	2453
Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu	
795 800 805	
gga atg gat tac ata gtc aag tct ctg tca agt gaa ccc tgt gac ctt	2501
Gly Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu	
810 815 820	
gaa gaa att caa tta gtc tcc tgc tgc ttg tct gca aat gca gtg aaa	2549
Glu Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys	
825 830 835	
atc cta gct cag aat ctt cac aat ttg gtc aaa ctg agc att ctt gat	2597
Ile Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp	
840 845 850	
tta tca gaa aat tac ctg gaa aaa gat gga aat gaa gct ctt cat gaa	2645
Leu Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu	
855 860 865 870	
ctg atc gac agg atg aac gtg cta gaa cag ctc acc gca ctg atg ctg	2693
Leu Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu	
875 880 885	

FIG. 1D

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ccc tgg ggc tgt gac gtg caa ggc agc ctg agc agc ctg ttg aaa cat	2741
Pro Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His	
890 895 900	
ttg gag gag gtc cca caa ctc gtc aag ctt ggg ttg aaa aac tgg aga	2789
Leu Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg	
905 910 915	
ctc aca gat aca gag att aga att tta ggt gca ttt ttt gga aag aac	2837
Leu Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn	
920 925 930	
cct ctg aaa aac ttc cag cag ttg aat ttg gcg gga aat cgt gtg agc	2885
Pro Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser	
935 940 945 950	
agt gat gga tgg ctt gcc ttc atg ggt gta ttt gag aat ctt aag caa	2933
Ser Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys Gln	
955 960 965	
tta gtg ttt ttt gac ttt agt act aaa gaa ttt cta cct gat cca gca	2981
Leu Val Phe Phe Asp Phe Ser Thr Lys Glu Phe Leu Pro Asp Pro Ala	
970 975 980	
tta gtc aga aaa ctt agc caa gtg tta tcc aag tta act ttt ctg caa	3029
Leu Val Arg Lys Leu Ser Gln Val Leu Ser Lys Leu Thr Phe Leu Gln	
985 990 995	
gaa gct agg ctt gtt ggg tgg caa ttt gat gat gat gat ctc agt gtt	3077
Glu Ala Arg Leu Val Gly Trp Gln Phe Asp Asp Asp Asp Leu Ser Val	
1000 1005 1010	
att aca ggt gct ttt aaa cta gta act gct taa ataaagtgtgta ctcgaagcca	3130
Ile Thr Gly Ala Phe Lys Leu Val Thr Ala *	
1015 1020	
gta	3133

FIG. 1E

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1 ATGCTGAACGCTGGTCCCCTGGGCTCCCTTATTTCTTTCTCTATACTTTGTCTCTGTGTCTTTTTCTTTTT
TACGACTTGCGACCAGGGGACCCGAGGGAATAAGAAAGAGATATGAAACAGAGACACAGAAAAAGAAAA
1▶ M L N A G P L G S L I S F S I L C L C V F F F
71 CCAAGTCTCTCGTTCCACCTAACGAGAAACACCCACAGAACAAGAAGGTATCTGGTCTACAAGAACTCGA
GGTTCAGAGAGCAAGGTGGATTGCTCTTTGTGGGTGTCTTGTCTTCCATAGACCAGATGTTCTTGAGCT
24▶ S K S L V P P N E K H P Q N K K V S G L Q E L E
141 GGCCTCACTGAAACGGAAAGCAAATACAAAGAAACTTTATTTTAAAAACATGTCTTGGTCTCCCAAGAAG
CCGGAGTGACTTTGCCTTTTCGTTTATGTTTCTTTGAAATAAAATTTTGTACAGAACCAGAGGGTTCTTC
47▶ A S L K R K A N T K K L Y F K N M S W S P K K
211 AGGGCAATTGGATTGCTCAGCCAGAGACCCTTGCAGGCAGACACACAAGCGGCTGGACGTCGAGAGGAAC
TCCCGTTAACCTAACGAGTCGGTCTCTGGGAACGTCGCTGTGTGTTTCGCCGACCTGCAGCTCTCCTTG
71▶ R A I G L L S Q R P L Q A D T Q A A G R R E E
281 ACATCGGCGGAAGAACATACAGCAGCTGGACGTCAGAGGACGTTGAAGGGAGAATGCTGGCGGAAGAG
TGTAGCCGCCCTTCTTGTATGTTTCGTCGACCTGCAGGTCTCCTGCAACTTCCCTCTTACGACCGCCTTCTC
94▶ H I G G R T Y K Q L D V Q R T L K G E C W R K S
351 CACACAACAGACATCGGCACGCCAGCAGGCCATCCACCAGAGGAACGACTCGGAGTTTGGCCTGGAGGTG
GTGTGTTGTCTGTAGCCGTCGCGTCCGTTAGGTGGTCTCCTTGTCTGAGCCTCAAACCGGACCTCCAC
117▶ T Q Q T S A R Q Q A I H Q R N D S E F G L E V
421 AATTTTCATAAAGGACAATAGCCGAGCCCTTATTTCAAAGAATGGGAATGACTGTTATAAAGCAAATCACAG
TTAAAGTATTTCTGTATCGGCTCGGGAATAAGTTTCTTACCCTTACTGACAATATTTTCGTTTGTAGTGT
141▶ N F I K D N S R A L I Q R M G M T V I K Q I T
491 ATGACCTATTTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATCATTTGCTGCGAGAAGGTGGAGCA
TACTGGATAAACATACCTTACAAGACTTAGCGCTTCTTTCATTTGTAGTAAACGACGCTCTTCCACCTCGT
164▶ D D L F V W N V L N R E E V N I I C C E K V E Q
561 GGATGCTGCTAGAGGGATCATTACATGATTTTGAAAAAGGGTTCAGAGTCCTGTAACCTCTTTCTTAAA
CCTACGACGATCTCCCTAGTAAGTGTACTAAAACCTTTTCCCAAGTCTCAGGACATTGGAGAAAGAAATTT
187▶ D A A R G I I H M I L K K G S E S C N L F L K
631 TCCCTTAAGGAGTGGAACCTATCCTCTATTTTCAGGACTTGAATGGACAAAGTTTTGAGGAGACACAGAATT
AGGGAATTCCTCACCTTGATAGGAGATAAAGTCCTGAACTTACCTGTTTCAAACTCCTCTGTGTCTTAA
211▶ S L K E W N Y P L F Q D L N G Q S F E E T Q N
701 GGGTCTTCTTTAACATCACCTCTTCTCTAATAGGTCTTTTTTCATCAGACATCAGAAGGAGACTTGGACGA
CCCAGAAGAAATTGTAGTGGAGAAGAGATTATCCAGAAAAAGTAGTCTGTAGTCTTCTCTGAACCTGCT
234▶ W V F F N I T S S L I G L F H Q T S E G D L D D
771 TTTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCTTGGTGAAGAT
AAACCGAGTCCTAAATTTCTGAAACATGGTATGGGGTAGAAAAGACTTGAAAATAGGGGAACCACTTCTA
257▶ L A Q D L K D L Y H T P S F L N F Y P L G E D

FIG. 2A

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841 ATTGACATTATTTTAACTTGAAAAGCACCTTCACAGAACCTGTCTGTGGAGGAAGGACCAACACCATC
TAAGTGTAAATAAAAATTGAACTTTTCGTGGAGTGTCTTTGGACAGGACACCTCCTTCCTGGTTGTGGTAG
281▶ I D I I F N L K S T F T E P V L W R K D Q H H

911 ACCGCGTGGAGCAGCTGACCCTGAATGGCCTCCTGCAGGCTCTTCAGAGCCCCCTGCATCATTGAAGGGGA
TGGCGCACCTCGTCGACTGGGACTTACCGGAGGACGTCCGAGAAAGTCTCGGGGACGTAGTAACCTTCCCCT
304▶ H R V E Q L T L N G L L Q A L Q S P C I I E G E

981 ATCTGGCAAAGGCAAGTCCACTCTGCTGCAGCGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAAGGCT
TAGACCGTTTCCGTTTCAGGTGAGACGACGTGCTTAAACGGTACGAGACCCCGAGGCCTTTTCAGTTCCGA
327▶ S G K G K S T L L Q R I A M L W G S G K C K A

1051 CTGACCAAGTTCAAATTCGTCTTCTTCTCCGTCTCAGCAGGGCCCCAGGGTGGACTTTTGTAAACCCCTCT
GACTGGTTCAAGTTTAAGCAGAAGAAGGAGGCAGAGTCTGCCGGTCCCACCTGAAAAACTTTGGGAGA
351▶ L T K F K F V F F L R L S R A Q G G L F E T L

1121 GTGATCAACTCCTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGCTGAAGCTGCG
CACTAGTTGAGGACCTATATGGACCGTGTAGTCTTCTGCTGTAAAGTACCGGTACGACGACTTCGACGC
374▶ C D Q L L D I P G T I R K Q T F M A M L L K L R

1191 GCAGAGGGTTCTTTTCTTCTTGATGGCTACAATGAATTCAAGCCCCAGAACTGCCAGAAATCGAAGCC
CGTCTCCCAAGAAAAGGAAGAACTACCGATGTTACTTAAAGTTCGGGGTCTTTGACGGGTCTTTAGCTTCGG
397▶ Q R V L F L L D G Y N E F K P Q N C P E I E A

1261 CTGATAAAGGAAAACACCGCTTCAAGAACATGGTCATCGTCACCACTACCACTGAGTGCCTGAGGCACA
GACTATTTCTTTTGGTGGCGAAGTCTTGTACCAGTAGCAGTGGTGATGGTGACTCACGGACTCCGTGT
421▶ L I K E N H R F K N M V I V T T T T E C L R H

1331 TACGGCAGTTTGGTGGCCCTGACTGCTGAGGTGGGGGATATGACAGAAGACAGCGCCCAGGCTCTCATCCG
ATGCCGTCAAACCAAGGACTGACGACTCCACCCCTATACTGTCTTCTGTGCGGGTCCGAGAGTAGGC
444▶ I R Q F G A L T A E V G D M T E D S A Q A L I R

1401 AGAAGTGCTGATCAAGGAGCTTGCTGAAGGCTTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAAT
TCTTCACGACTAGTTCTCGAAGGACTTCCGAACAACGAGGTTTAAGTCTTTAGGTCCACGAACCTCTTA
467▶ E V L I K E L A E G L L L Q I Q K S R C L R N

1471 CTCATGAAGACCCCTCTCTTTGTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTC
GAGTACTTCTGGGGAGAGAAACACCACTAGTGAACACGTTAGGTCTACCCACTTTCACTCAAGGTGAGAG
491▶ L M K T P L F V V I T C A I Q M G E S E F H S

1541 ACACACAAACAACGCTGTTCCATACCTTCTATGATCTGTTGATACAGAAAAACAAACACAAACATAAAGG
TGTGTGTTTGTGCGACAAGGTATGGAAGATACTAGACAACCTATGTCTTTTGTGTTGTGTTGTATTTC
514▶ H T Q T T L F H T F Y D L L I Q K N K H K H K G

1611 TGTGGCTGCAAGTGACTTCATTCGGAGCCTGGACCACTGTGGAGACCTAGCTCTGGAGGGTGTGTTCTCC
ACACCGACGTTCACTGAAGTAAGCCTCGACCTGGTGACACCTCTGGATCGAGACCTCCACACAAGAGG
537▶ V A A S D F I R S L D H C G D L A L E G V F S

1681 CACAAGTTTGATTTCGAAGTGCAGGATGTGTCCAGCGTGAATGAGGATGTCTCTGCTGACAACCTGGGCTCC
GTGTTCAAACCTAAAGCTTGACGTCTACACAGGTGCGCACTTACTCCTACAGGACGACTGTTGACCCGAGG
561▶ H K F D F E L Q D V S S V N E D V L L T T G L

FIG. 2B

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1751 TCTGTAAATATACAGCTCAAAGGTTCAAGCCAAAGTATAAAATCTTTTCAAGTCATTCCAGGAGTACAC
AGACATTTATATGTCGAGTTTCCAAGTTTCGGTTTCATATTTAAGAAAGTGTTCAGTAAGGTCCTCATGTG
584▶ L C K Y T A Q R F K P K Y K F F H K S F Q E Y T

1821 AGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGGTTAC
TCGTCTTGCTTCTGAGTCGTCAAATAACTGCAGAGTACTCGGTCTCCTCCACTGGTTCCCTTACCAATG
607▶ A G R R L S S L L T S H E P E E V T K G N G Y

1891 TTGCAGAAAATGGTTTCCATTTCCGACATTACATCCACTTATAGCAGCCTGCTCCGGTACACCTGTGGGT
AACGTCTTTTACCAAAGGTAAAGCCTGTAATGTAGGTGAATATCGTCCGACGAGGCCATGTGGACACCCA
631▶ L Q K M V S I S D I T S T Y S S L L R Y T C G

1961 CATCTGTGGAAGCCACCAGGGCTGTTATGAAGCACCTCGCAGCAGTGTATCAACACGGCTGCCTTCTCGG
GTAGACACCTTCCGTGGTCCCGACAATACTTCGTGGAGCGTCGTACATAGTTGTGCCGACGGAAGAGCC
654▶ S S V E A T R A V M K H L A A V Y Q H G C L L G

2031 ACTTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTTTGCAAAGTGTGAAAAACACCACTGAGCAA
TGAAAGGTAGCGGTTCTCCGGAGAGACCTCTGTCTCTTAGAAACGTTTCACACTTTTGTGGTGA CTGTT
677▶ L S I A K R P L W R Q E S L Q S V K N T T E Q

2101 GAAATTCGAAAGCCATAAACATCAATTCCTTTGTAGAGTGTGGCATCCATTTATATCAAGAGAGTACAT
CTTTAAGACTTTTCGGTATTTGTAGTTAAGGAAACATCTCACACCGTAGGTAAATATAGTTCTCTCATGTA
701▶ E I L K A I N I N S F V E C G I H L Y Q E S T

2171 CCAAATCAGCCCTGAGCCAAGAATTTGAAGCTTTCTTTCAAGGTAAAAGCTTATATATCAACTCAGGGAA
GGTTTGTAGTCGGGACTCGGTTCTTAAACTTCGAAAGAAAGTTCCATTTTCGAATATATAGTTGAGTCCCTT
724▶ S K S A L S Q E F E A F F Q G K S L Y I N S G N

2241 CATCCCCGATTACTTATTGACTTCTTTGAACATTTGCCCAATTGTGCAAGTGCCCTGGACTTCATTAAA
GTAGGGGCTAATGAATAAACTGAAGAACTTGTAAACGGGTTAACACGTTTCACGGGACCTGAAGTAATTT
747▶ I P D Y L F D F F E H L P N C A S A L D F I K

2311 CTGGACTTTTATGGGGGAGCTATGGCTTCATGGGAAAAAGGCTGCAGAAGACACAGGTGGAATCCACATGG
GACCTGAAAATACCCCTCGATACCGAAGTACCCCTTTTCCGACGCTTCTGTGTCCACCTTAGGTGTACC
771▶ L D F Y G G A M A S W E K A A E D T G G I H M

2381 AAGAGGCCCCAGAAACCTACATTCCCAGCAGGGCTGTATCTTTGTCTTTCAACTGGAAGCAGGAATTCAG
TTCTCCGGGGTCTTTGGATGTAAGGGTCGTCCCGACATAGAAACAAGAAGTTGACCTTCGTCTTAAAGTC
794▶ E E A P E T Y I P S R A V S L F F N W K Q E F R

2451 GACTCTGGAGGTACACTCCGGGATTTTCAGCAAGTTGAATAAGCAAGATATCAGATATCTGGGGAAAATA
CTGAGACCTCCAGTGTGAGGCCCTAAAGTCGTTCAACTTATTCGTTCTATAGTCTATAGACCCCTTTTAT
817▶ T L E V T L R D F S K L N K Q D I R Y L G K I

2521 TTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCTCAGTTTGG
AAGTCGAGACGGTGTTCGAGTCCGACGTTTATTCTCTACACGACCACACCGACCTTCGGAGTCAAACC
841▶ F S S A T S L R L Q I K R C A G V A G S L S L

2591 TCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTGGAAAGCCAGTCCCTCACCATAGAAGATGAGAG
AGGAGTCGTGGACATTCTGTAAATAAGAGAGTACCACCTTCGGTCAGGGGAGTGGTATCTTCTACTCTC
864▶ V L S T C K N I Y S L M V E A S P L T I E D E R

FIG. 2C

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2661 GCACATCACATCTGTAAACAAACCTGAAAACCTTGAGTAATTCATGACCTACAGAATCAACGGCTGCCGGGT
CGTGTAGTGTAGACATTGTTTGGACTTTTGGAACTCATAAGTACTGGATGTCTTAGTTGCCGACGGCCCA
887▶ H I T S V T N L K T L S I H D L Q N Q R L P G
2731 GGTCTGACTGACAGCTTGGGTAACCTTGAAGAACCTTACAAAGCTCATAATGGATAACATAAAGATGAATG
CCAGACTGACTGTGGAACCCATTTGAACCTTCTTGGGAATGTTTCGAGTATTACCTATTGTATTTCTACTTAC
911▶ G L T D S L G N L K N L T K L I M D N I K M N
2801 AAGAAGATGCTATAAACTAGCTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTTATTTTCATTTGACCCA
TTCTTTCTACGATATTTTGATCGACTTCCGGACTTTTGGACTTCTTCTACACAAATAAAGTAAACTGGGT
934▶ E E D A I K L A E G L K N L K K M C L F H L T H
2871 CTTGTCTGACATTGGAGAGGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGACCTTGAA
GAACAGACTGTAACCTCTCCCTTACCTAATGTATCAGTTTCAGAGACAGTTCACTTGGGACACTGGAACTT
957▶ L S D I G E G M D Y I V K S L S S E P C D L E
2941 GAAATTCAAATTAGTCTCTCTGCTGCTTGTCTGCAAAATGCAGTGAAAAATCCTAGCTCAGAAATCTTCACAAAT
CTTTAAGTTAATCAGAGGACGACGAACAGACGTTTACGTCACTTTTAGGATCGAGTCTTTAGAAGTGTTAA
981▶ E I Q L V S C C L S A N A V K I L A Q N L H N
3011 TGGTCAAACCTGAGCATTCTTTGATTTATCAGAAAAATACCTGGAAAAAGATGGAAATGAAGCTCTTCATGA
ACCAGTTTGACTCGTAAGAACTAAATAGTCTTTTAAATGGACCTTTTTCTACCTTTACTTTCGAGAAAGTACT
1004▶ L V K L S I L D L S E N Y L E K D G N E A L H E
3081 ACTGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAA
TGACTAGCTGTCTACTTGCACGATCTTGTGCGAGTGGCGTGACTACGACGGGACCCCGACACTGCACGTT
1027▶ L I D R M N V L E Q L T A L M L P W G C D V Q
3151 GGCAGCCTGAGCAGCCTGTTTGAAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACT
CCGTCGGACTCGTCGGACAACCTTTGTAAACCTCTCCAGGGTGTGTGAGCAGTTTGAACCCCAACTTTTGA
1051▶ G S L S S L L K H L E E V P Q L V K L G L K N
3221 GGAGACTCACAGATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGAACCCTCTGAAAAACTTTCCA
CCTCTGAGTGTCTATGTCTCTAATCTTAAATCCACGTAAAAAACCTTTCTTGGGAGACTTTTGAAGGT
1074▶ W R L T D T E I R I L G A F F G K N P L K N F Q
3291 GCAGTTGAATTTGGCGGGAAATCGTGTGAGCAGTGATGGATGGCTTGCCTTCATGGGTGTATTTGAGAAT
CGTCAACTTAAACCGCCCTTTAGCACACTCGTCACTACCTACCGAACGGAAGTACCCACATAAACTCTTA
1097▶ Q L N L A G N R V S S D G W L A F M G V F E N
3361 CTTAAGCAATTAGTGTTTTTTGGACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAAAC
GAATTCGTTAATCACAATAAACTGAAATCATGATTTCTTAAAGATGGACTAGGTTCGTAATCAGTCTTTTG
1121▶ L K Q L V F F D F S T K E F L P D P A L V R K
3431 TTAGCCAAGTGTTATCCAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTGGGTGGCAATTTGATGATGA
AATCGGTTTACAATAGGTTCAATTGAAAAGACGTTCTTCGATCCGAACAACCCACCGTTAAACTACTACT
1144▶ L S Q V L S K L T F L Q E A R L V G W Q F D D D
3501 TGATCTCAGTGTTATTACAGATGAGAAAGCTCAGATGATTTGCCCATGGGTTATAAACTACTTCTTTAC
ACTAGAGTCACAATAATGTCTACTCTTTTCGAGTCTACTAAACGGGTACCCAATATTTTGTATGAAGGAATG
1167▶ D L S V I T D E K A Q M I C P W V I K L L P Y

FIG. 2D

3571 ACAGTGGCAGCATCAGAACTGGAATTCAGATCTCTTGCCTCCTAG
TGTCACCGTCGTAGTCTTGACCTTAAGTCTAGAGAACGGAGGATC
1191 T V A A S E L E F R S L A S

FIG. 2E

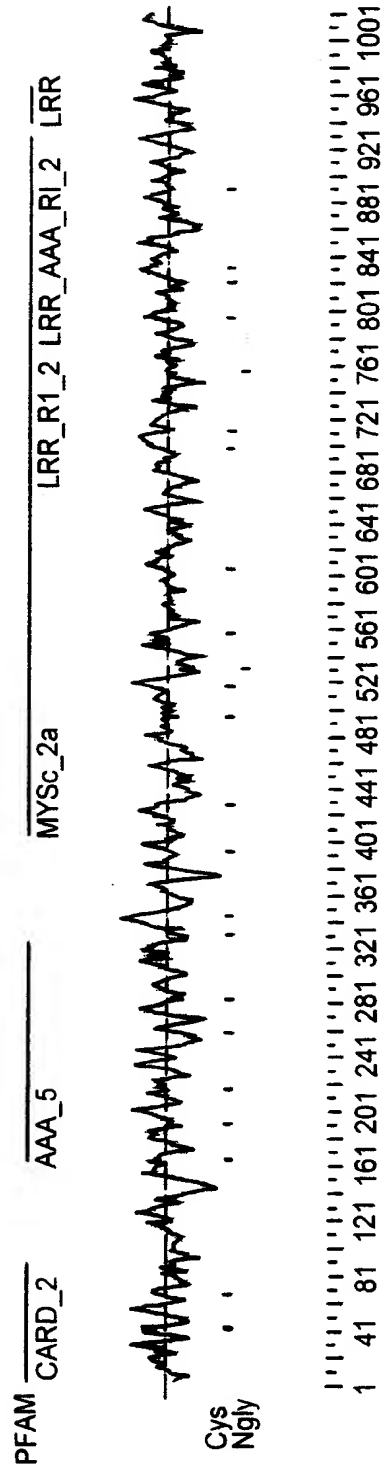
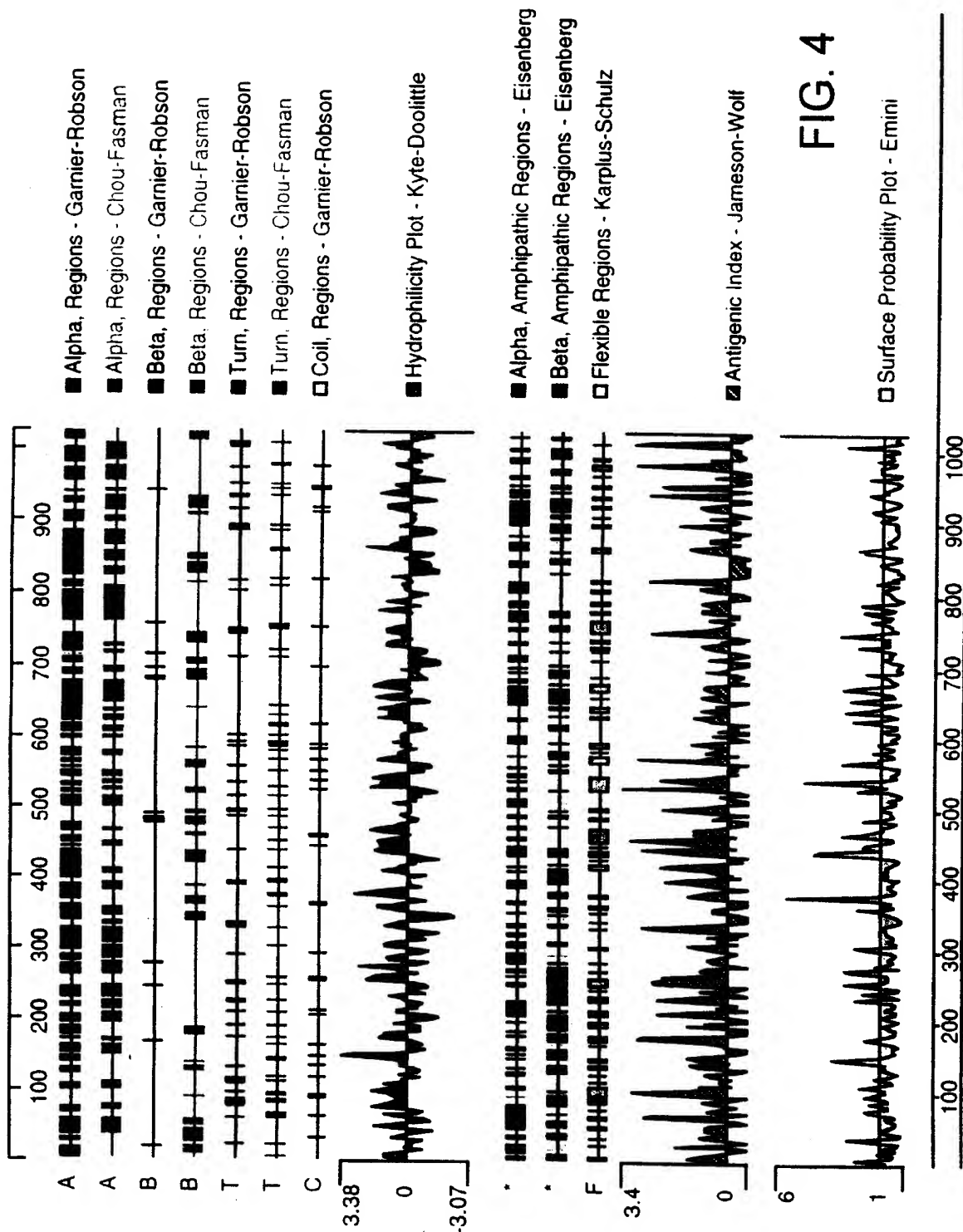


FIG. 3



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CARD: domain 1 of 1, from 2 to 88: score 16.0, E = 0.0065
 *->aeddrlllrknrllellgeltlsglLdhLleknlvLteeeeeEkikaknt
 + ++ ++ + +g +++++ d+L nvL+ee+ i +
CARD12 2 --NFIKDNSRALIQRMGMTVIKQITDDLFWVWNLNREEVNIICCEKV 46
 trrdkareLiDsvqkkGnqAfqiFlqaLretdqelladlllde<-*
 ++ d ar i +++kkG++ ++F1 +L+e ++ l +dl +
CARD12 47 EQ-DAARGIIHMILKKGSESCNLFKSLKEWNYPLFQDLNGQS 88

FIG. 5A

LRR: domain 1 of 4, from 764 to 791: score 0.6, E = 8.2e+02
 ->nLeeLdLsnN.Lt.....slppglfsnLp<-
 nL++L ++n + +++ +l +g ++nL+
CARD12 764 NLTKLIMDNikMNeedaiKLAEG-LKNLK 791 **FIG. 5B**

LRR: domain 2 of 4, from 821 to 848: score 0.3, E = 9.3e+02
 ->nLeeLdLsnN.Lt.....slppglfsnLp<-
 Lee+ L ++ L+ + ++ ++nL
CARD12 821 DLEEIQLVSCcLSanavKILAQNLHNLV 848 **FIG. 5C**

LRR: domain 3 of 4, from 849 to 872: score 11.2, E = 23
 ->nLeeLdLsnN.LtslppglfsnLp<-
 +L LdLs N L++ +++++ L
CARD12 849 KLSILDLSENyLEKDGNEALHELI 872 **FIG. 5D**

LRR: domain 4 of 4, from 938 to 965: score 4.2, E = 2.5e+02
 ->nLeeLdLsnN.Lt.....slppglfsnLp<-
 n + L+L +N+ +++++ + +f+nL+
CARD12 938 NFQQLNLAGNrVSSdgwlAFMG-VFENLK 965
FIG. 5E

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	E . L . L L . S E G E . G . G K . . . L L . . I A . L W . S G	Consensus #1
	E Q L V L N G V L G A L N S V C I V E G E A G S G K S V L L Q K I A F L W G S G	Majority
	10 20 30 40	
1	E Q L T L N G L L Q A L Q S P C I I E G E S G K G K S T L L Q R I A M L W G S G	CARD12-C
1	E P L V L P E V F G N L N S V M C V E G E A G S G K T V L L K K I A F L W A S G	NATP-C
	. C . . L . . F . . V F . L . L S . . R G L C D Q L L . . . G . .	Consensus #1
	K C K A L T K F Q L V F F L S L S S T R A D G G L A S I L C D Q L L D I E G S V	Majority
	50 60 70 80	
41	K C K A L T K F K F V F F L R L S - - R A Q G G L F E T L C D Q L L D I P G T I	CARD12-C
41	C C P L L N R E Q L V F Y L S L S S T R P D E G L A S I I C D Q L L E K E G S V	NATP-C
 L . . . V L F L L D . Y . E C I . . L	Consensus #1
	T E Q T F R A I L L Q L K N Q V L F L L D G Y N E I K P O N C S I P Q V I G A L	Majority
	90 100 110 120	
79	R K Q T F M A M L L K L R Q R V L F L L D G Y N E F K P Q N C P E - - - I E A L	CARD12-C
81	T E M C M R N I I Q Q L K N Q V L F L L D D Y K E I - - - C S I P Q V I G K L	NATP-C
	I . . N H T . . . R . I R E	Consensus #1
	I Q E N H L S K T C V L V A V T T E R A R D I R O F G A L I A E V G A F T E D S	Majority
	130 140 150 160	
116	I K E N H R F K N M V I V T T T T E C L R H I R Q F G A L T A E V G D M T E D S	CARD12-C
117	I Q K N H L S R T C L L I A V R T N R A R D I R R Y L E T I L E I Q A F P F Y N	NATP-C
 R K L K T P L F V .	Consensus #1
	A V A L L R E V L I K E L A E L R G L L V Q I G K S Q S L Q N L Q K T P L F V A	Majority
	170 180 190 200	
156	A Q A L I R E V L I K E L A E - - G L L L Q I Q K S R C L R N L M K T P L F V V	CARD12-C
157	T V C I L R K L F S H N M T R L R K F M V Y F G K N Q S L Q K I Q K T P L F V A	NATP-C
	. . C A F F L N K	Consensus #1
	A I C A I Q W G E S E F D S S F T D V A V F K S F Y D L L I L K N K H K H K G V	Majority
	210 220 230 240	
194	I T C A I Q M G E S E F H S H - T Q T T L F H T F Y D L L I Q K N K H K H K G V	CARD12-C
197	A I C A - H W F Q Y P F D P S F D D V A V F K S Y M E R L S L R N K - - - - -	NATP-C
	A C G . L A L . G . F S . . F . F D V . E	Consensus #1
	A A A D I L K A T V S S C G D L A L E G V F S H K F D F E L D D V A E A G V D E	Majority
	250 260 270 280	
233	A A S D F I R S - L D H C G D L A L E G V F S H K F D F E L Q D V S - - S V N E	CARD12-C
230	A T A E I L K A T V S S C G E L A L K G F F S C C F E F N D D D L A E A G V D E	NATP-C
	D . . L T . . L . . K . T A Q R . . P . Y . F F Q E . . A G . R L . . L	Consensus #1
	D V L L T T G L L S K F T A Q R L K P K Y K F L S K A F Q E F L A G R R L I S L	Majority
	290 300 310 320	
270	D V L L T T G L L C K Y T A Q R F K P K Y K F F H K S F Q E Y T A G R R L S S L	CARD12-C
270	D E D L T M C L M S K F T A Q R L R P F Y R E L S P A F O E F L A G M R L I E L	NATP-C

FIG. 6A

	610	620	630	640
578	E D E R H I T S V T N L K T L S	I H D L Q N Q R L P G G L	T D S L G N L K N L T	CARD 12

FIG. 6B

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	..I.....K.....C.....LS.....	Consensus #1
	ELIRDALELSEASAIKLAEGCLKNLKKMCLISLLELSAAGE	Majority
	650 660 670 680	
618	KLIMDNIKMNEEDAIKLAEGCLKNLKKMCLFHLTHLSLDIGE	CARD12-C
592	ESIRPALELSKASVTK-----CSISKLELSAAEQ	NAIP-C
SL.S.....LE.....Q.....N	Consensus #1
	GLLLIVKSLSSSEPCDLEEIQLVSCCLVAGAVQILAQILHN	Majority
	690 700 710 720	
658	GMDYIVKSLSSSEPCDLEEIQLVSCCLSANAVKILAQNLHN	CARD12-C
621	ELLLTLPLSLES-----LE-----VSGTIQSQDQIFPN	NAIP-C
	L.K...L.L.E.....GN.....I.....L.	Consensus #1
	LVKLSILDLSSELSVDLDGNIAVHSVIVPDEFNVLEQLTALL	Majority
	730 740 750 760	
698	LVKLSILDLSENYLEKDGNEALHELI-DRMNVLEQLTALM	CARD12-C
648	LDKF--LCLKELSVLDLEGNINVFSVIPEEFPNFHHMEKLL	NAIP-C
S.L...L.....L.L.L.....D.E..	Consensus #1
	LQIGADV DGSLSLSSLVASLEEVISLVILGLEGOQLTDTEIS	Majority
	770 780 790 800	
737	LPWGC DVQGSLSLSLKHL EEPQLVKLG LKNWRLTDTEIR	CARD12-C
686	IQISA EYDP--SKLVASLPNFISLKI LNLEGOQFPDEETS	NAIP-C
	...A.....L.N...L.L.....G.....K	Consensus #1
	ILGAFIGLGSLSNLEELILAGGDVSSDGWLAFMGVFEVAK	Majority
	810 820 830 840	
777	ILGAFFGKNPLKKNFQQNLNLAGNRVSSDGWLAFMGVFNELK	CARD12-C
724	EKFAYI-LGSLSNLEELIILPTGD-----GIYRVAK	NAIP-C
	..LVFFDFSTKEFLPDPALVQQLSQVLSVLSFLQTLARLVGW	Consensus #1
	850 860 870 880	Majority
817	QLVFFDFSTKEFLPDPALVRKLSQVLSKLTFLQEARLVGW	CARD12-C
753	LII-----QQCQQL-HCLRVLSFFKT-----	NAIP-C
	...DD...I.....	Consensus #1
	QLDDDSVVVITGAFKLVTA	Majority
	890	
857	QFDDDDL SVITGAFKLVTA	CARD12-C
773	-LND DSVVEI-----G	NAIP-C

Consensus 'Consensus #1': When all match the residue of CARD12-C show the residue of CARD12-C, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #1' exactly.

FIG. 6C